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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/12, C07K 14/705, C12N 5/10, 15/57, 9/48, 9/14, 15/55</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 98/21328</b> <b>(43) International Publication Date:</b> 22 May 1998 (22.05.98)
<b>(21) International Application Number:</b> PCT/JP97/04056 <b>(22) International Filing Date:</b> 7 November 1997 (07.11.97) <b>(30) Priority Data:</b> 8/301429 13 November 1996 (13.11.96) JP <b>(71) Applicants (for all designated States except US):</b> SAGAMI CHEMICAL RESEARCH CENTER [JP/JP]; 4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229 (JP). PROTEGENE INC. [JP/JP]; 2-20-3, Naka-cho, Meguro-ku, Tokyo 153 (JP). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> KATO, Seishi [JP/JP]; 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229 (JP). SEKINE, Shingo [JP/JP]; 4-4-1, Nishi-Ohnuma, Sagamihara-shi, Kanagawa 229 (JP). YAMAGUCHI, Tomoko [JP/JP]; 5-13-11, Takasago, Katsushika-ku, Tokyo 125 (JP). KOBAYASHI, Midori [JP/JP]; 647-2, Chougo, Fujisawa-shi, Kanagawa 252 (JP). <b>(74) Agents:</b> AOYAMA, Tamotsu et al.; Aoyama & Partners, IMP Building, 3-7, Shiromi 1-chome, Chuo-ku, Osaka-shi, Osaka 540 (JP).		<b>(81) Designated States:</b> AU, CA, JP, MX, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> <b>(88) Date of publication of the international search report:</b> 20 August 1998 (20.08.98)
<b>(54) Title:</b> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs ENCODING THESE PROTEINS		
<b>(57) Abstract</b> <p>Proteins containing any of the amino acid sequences represented by Sequence No. 1 to Sequence No. 2 or by Sequence No. 4 to Sequence No. 25 and DNAs encoding said proteins exemplified by cDNAs containing any of the base sequences represented by Sequence No. 26 to Sequence No. 50. Said proteins can be provided by expressing cDNAs encoding human proteins having transmembrane domains and recombinants of these human cDNAs.</p>		

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# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/JP 97/04056

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/705 C12N5/10 C12N15/57 C12N9/48  
C12N9/14 C12N15/55

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	JOURNAL OF MOLECULAR BIOLOGY, vol. 157, no. 1, 5 May 1982, pages 105-132, XP000609692 KYTE J ET AL: "A SIMPLE METHOD FOR DISPLAYING THE HYDROPATHIC CHARACTER OF A PROTEIN" cited in the application see abstract	1-5
Y	SCIENCE, vol. 272, 10 May 1996, pages 872-877, XP002031517 FENG Y ET AL: "HIV-1 ENTER COFACTOR: FUNCTIONAL CDNA CLONING OF A SEVEN-TRANSMEMBRANE G PROTEIN-COUPLED RECEPTOR" cited in the application see the whole document	1-5

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☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

\* Special categories of cited documents:

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"P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

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Date of the actual completion of the international search

12 March 1998

Date of mailing of the international search report

03.07.98

Name and mailing address of the ISA

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# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/JP 97/04056

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	J BIOL CHEM, APR 12 1996, 271 (15) P8549-52, UNITED STATES, XP002058790 HOLLOWAY MP ET AL: "A hydrophobic domain of Ca <sup>2+</sup> -modulating cyclophilin ligand modulates calcium influx signaling in T lymphocytes." see abstract	1-5
Y	--- BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS., vol. 168, 1990, ORLANDO, FL US, pages 574-579, XP002058791 APPERSON M ET AL: "A yeast protein, homologous to the proteolipid of the chromaffin granule proton-ATPase, is important for cell growth" see figure 2	1-5
P,X	--- EMHUM1 Database entry HSD052 Accession number D89052; 07 Dec 1996 NISHIGORI H ET AL: 'Cloning and chromosomal localization of the gene encoding a protein homologous to the yeast protein PPA1, an proton-ATPase-like protein' XP002058792 see sequence -----	1-5

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP 97/ 04056

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see continuation-sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-5 in part (subject 1. on next sheet)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International Application No. PCT/JP 97/04056

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 26 and 51 and protein relating to  
SEQ ID No 1

2. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 27 and 52 and protein relating to  
SEQ ID No 2

3. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 28 and 53 and protein relating to  
SEQ ID No 3

4. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 29 and 54 and protein relating to  
SEQ ID No 4

5. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 30 and 55 and protein relating to  
SEQ ID No 5

6. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 31 and 56 and protein relating to  
SEQ ID No 6

7. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 32 and 57 and protein relating to  
SEQ ID No 7

8. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 33 and 58 and protein relating to  
SEQ ID No 8

9. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 34 and 59 and protein relating to  
SEQ ID No 9

10. Claims: Claims 1-5 in part

# INTERNATIONAL SEARCH REPORT

International Application No. PCT/ JP 97/04056

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

DNAs relating to SEQ ID No 35 and 60 and protein relating to  
SEQ ID No 10

11. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 36 and 61 and protein relating to  
SEQ ID No 11

12. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 37 and 62 and protein relating to  
SEQ ID No 12

13. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 38 and 63 and protein relating to  
SEQ ID No 13

14. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 39 and 64 and protein relating to  
SEQ ID No 14

16. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 41 and 66 and protein relating to  
SEQ ID No 16

17. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 42 and 67 and protein relating to  
SEQ ID No 17

18. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 43 and 68 and protein relating to  
SEQ ID No 18

19. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 44 and 69 and protein relating to  
SEQ ID No 19

20. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 45 and 70 and protein relating to  
SEQ ID No 20

## INTERNATIONAL SEARCH REPORT

International Application No. PCT/ JP 97/04056

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

21. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 46 and 71 and protein relating to  
SEQ ID No 21

22. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 47 and 72 and protein relating to  
SEQ ID No 22

23. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 48 and 73 and protein relating to  
SEQ ID No 23

24. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 49 and 74 and protein relating to  
SEQ ID No 24

25. Claims: Claims 1-5 in part

DNAs relating to SEQ ID No 50 and 75 and protein relating to  
SEQ ID No 25



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TCATGCACCC TGTACAGTTG CCACGTTACT GCCTTTTTTA AAAATATATT TGACAGAAAC 1690  
 CAGGTGCCTT CAGAGGCTCT CTGATTAA T 1721

Sequence No.: 68

Sequence length: 1504

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10297

Sequence characteristics

Code representing characteristics: CDS

Existence site: 63.. 614

Characterization method: E

Sequence description

CTTTTGC GGC TGCAGCGGGC TTGTAGGTGT CCGGCTTTGC TGGCCCAGCA AGCCTGATAA 60  
 GC ATG AAG CTC TTA TCT TTG GTG GCT GTG GTC GGG TGT TTG CTG GTG 107  
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
 1 5 10 15  
 CCC CCA GCT GAA GCC AAC AAG AGT TCT GAA GAT ATC CGG TGC AAA TGC 155  
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys  
 20 25 30  
 ATC TGT CCA CCT TAT AGA AAC ATC AGT GGG CAC ATT TAC AAC CAG AAT 203  
 Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn  
 35 40 45  
 GTA TCC CAG AAG GAC TGC AAC TGC CTG CAC GTG GTG GAG CCC ATG CCA 251  
 Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro  
 50 55 60  
 GTG CCT GGC CAT GAC GTG GAG GCC TAC TGC CTG CTG TGC GAG TGC AGG 299  
 Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg  
 65 70 75  
 TAC GAG GAG CGC AGC ACC ACC ACC ATC AAG GTC ATC ATT GTC ATC TAC 347  
 Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr  
 80 85 90 95  
 CTG TCC GTG GTG GGT GCC CTG TTG CTC TAC ATG GCC TTC CTG ATG CTG 395  
 Leu Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu  
 100 105 110  
 GTG GAC CCT CTG ATC CGA AAG CCG GAT GCA TAC ACT GAG CAA CTG CAC 443  
 Val Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His

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115	120	125	
AAT GAG GAG GAG AAT GAG GAT GCT CGC TCT ATG GCA GCA GCT GCT GCA			491
Asn Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala			
130	135	140	
TCC CTC GGG GGA CCC CGA GCA AAC ACA GTC CTG GAG CGT GTG GAA GGT			539
Ser Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly			
145	150	155	
GCC CAG CAG CGG TGG AAG CTG CAG GTG CAG GAG CAG CGG AAG ACA GTC			587
Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val			
160	165	170	175
TTC GAT CGG CAC AAG ATG CTC AGC TAGATGGGCT GGTGTGGTTG GGTCAAGGC			640
Phe Asp Arg His Lys Met Leu Ser			
180			
CCCAACACCA TGGCTGCCAG CTTCCAGGCT GGACAAAGCA GGGGGCTACT TCTCCCTTCC			700
CTCGGTTCCA GTCTTCCCTT TAAAAGCCTG TGGCATTTTT CCTCCTTCTC CCTAACTTTA			760
GAAATGTTGT ACTTGGCTAT TTTGATTAGG GAAGAGGGAT GTGGTCTCTG ATCTCTGTTG			820
TCTTCTTGGG TCTTTGGGGT TGAAGGGAGG GGAAGGCAG GCCAGAAGGG AATGGAGACA			880
TTCCAGGCGG CCTCAGGAGT GGATGCGATC TGTCTCTCCT GGCTCCACTC TTGCCGCCTT			940
CCAGCTCTGA GTCTTGGGAA TGTGTGTTACC CTTGGAAGAT AAAGCTGGGT CTTCAGGAAC			1000
TCAGTGTCTG GGAGGAAAGC ATGGCCCAGC ATTGAGCATG TGTTCCTTTC TGCAGTGGTT			1060
CTTATCACCA CCTCCCTCCC AGCCCCAGCG CCTCAGCCCC AGCCCCAGCT CCAGCCCTGA			1120
GGACAGCTCT GATGGGAGAG CTGGGCCCCC TGAGCCCACT GGGTCTTCAG GGTGCACTGG			1180
AAGCTGGTGT TCGCTGTCCC CTGTGCACTT CTCGCACTGG GGCATGGAGT GCCCATGCAT			1240
ACTCTGCTGC CGGTCCCCTC ACCTGCACTT GAGGGGTCTG GGCAGTCCCT CCTCTCCCA			1300
GTGTCCACAG TCACTGAGCC AGACGGTCGG TTGGAACATG AGACTCGAGG CTGAGCGTGG			1360
ATCTGAACAC CACAGCCCCT GTACTTGGGT TGCCTCTTGT CCCTGAACTT CGTTGTACCA			1420
GTGCATGGAG AGAAAAATTTT GTCCTCTTGT CTTAGAGTTG TGTGTAAATC AAGGAAGCCA			1480
TCATTAAATT GTTTTATTTT TCTC			1504

Sequence No.: 69

Sequence length: 532

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10299

Sequence characteristics

Code representing characteristics: CDS

Existence site: 93.. 443

Characterization method: E

## Claims

1. A protein containing any of the amino acid sequences represented by Sequence No. 1 to Sequence No. 2 or by Sequence No. 4 to Sequence No. 25.

2. A DNA encoding any of the proteins as described in Claim 1.

3. A cDNA containing any of the base sequences represented by Sequence No. 26 to Sequence No. 50.

4. A cDNA as described in Claim 3 which comprises any of the base sequences represented by Sequence No. 51 to Sequence No. 75.

5. A transformed eukaryotic cell capable of expressing any of DNAs as described in Claim 2 to 4 and producing a protein as described in Claim 1.



Qy	661	AGGCTGGACAAAGCAGGGGGCTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAA	720
Db	666	AGGCTGGACAAAGCAGGGGGCTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAA	725
Qy	721	GCCTGTGGCATTTTTCTCCTTCTCCCTAACTTTAGAAATGTTGTA	780
Db	726	GCCTGTGGCATTTTTCTCCTTCTCCCTAACTTTAGAAATGTTGTA	785
Qy	781	TTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAG	840
Db	786	TTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAG	845
Qy	841	GGATGGGGAAGGCAGGCCAGAAAGGGAATGGAGACATTCGAGGCGGCCTCAGGAGTGGATG	900
Db	846	GGAGGGGGAAGGCAGGCCAGAAAGGGAATGGAGACATTCGAGGCGGCCTCAGGAGTGGATG	905
Qy	901	CGATCTGTCTCTCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGAATGTTG	960
Db	906	CGATCTGTCTCTCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGAATGTTG	965
Qy	961	TTACCCTTGGAAGATAAAGCTGGGTCTTCAGGAACCTCAGTGTCTGGGAGGAAAGCATGGC	1020
Db	966	TTACCCTTGGAAGATAAAGCTGGGTCTTCAGGAACCTCAGTGTCTGGGAGGAAAGCATGGC	1025
Qy	1021	CCAGCATTACAGCATGTGTTCTTTCTGCAGTGGTCTTATCACCACCTCCCTCCCAGCCC	1080
Db	1026	CCAGCATTACAGCATGTGTTCTTTCTGCAGTGGTCTTATCACCACCTCCCTCCCAGCCC	1085
Qy	1081	CAGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGGG	1140
Db	1086	CAGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGGG	1145
Qy	1141	CCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGAAGCTGGTGTTCGCTGTCCCCTGTG	1200
Db	1146	CCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGAAGCTGGTGTTCGCTGTCCCCTGTG	1205
Qy	1201	CACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACTCTGCTGCCGGTCCCCTCACCTG	1260
Db	1206	CACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACTCTGCTGCCGGTCCCCTCACCTG	1265
Qy	1261	CACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTCCACAGTCACTGAGCCAGACG	1320
Db	1266	CACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTCCACAGTCACTGAGCCAGACG	1325
Qy	1321	GTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAACACCACAGCCCCTGTACT	1380
Db	1326	GTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAACACCACAGCCCCTGTACT	1385
Qy	1381	TGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGAGAGAAAATTTTGTCTCT	1440
Db	1386	TGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGAGAGAAAATTTTGTCTCT	1445
Qy	1441	CTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTGTTTTATTTCTCTC	1499
Db	1446	CTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTGTTTTATTTCTCTC	1504